

We would like to thank Marek Stibal for taking the time to review the manuscript and for providing very relevant and constructive comments – please find responses to each below.

First, the results of microbiological analysis should be showed and discussed in more detail (e.g. how many raw sequences were obtained and how did that change after rarefaction; how many OTUs were identified and were the dominant OTUs similar to those of other glacial environments; was microbial abundance in the samples quantified in any way?).

Response: Microbial abundance in the samples were not quantified. We have included a sentence in Methods/Data Processing and Statistical Analyses to include the min (7,608) and max (188,117) number of raw reads per sample and the number of reads after rarefaction (7,608). We also added to the Results/Microbial assemblage the total number of OTUs identified across the rarefied dataset (3,555 OTUs) and material was added to the Discussion/Microbial assemblage to relate dominant OTUs to those identified in other glacial environments and prior literature: “Like glacier ice, the microbial assemblages observed in cold basal ice included Proteobacteria (\bar{x} = 42%), Bacteroidetes (\bar{x} =16%), Actinobacteria (\bar{x} =15%) and Cyanobacteria (\bar{x} = 7.8%) (Table 1). Proteobacteria, Bacteroidetes, Actinobacteria, and Cyanobacteria commonly dominate the microbiome of surface environments such as cryoconite holes (e.g. Cameron et al., 2012), glacier ice (e.g. Christner et al., 2005) and snow (e.g. Harding et al., 2011), and Cyanobacteria, Proteobacteria, and Actinobacteria contain organisms with the potential to photosynthesise (Cameron et al., 2012).” [...] “The microbial assemblages observed in warm basal ice were dominated by Proteobacteria (\bar{x} =30%) and Actinobacteria (\bar{x} =30%) which are commonly observed in cold ecosystems (Amato et al. 2007; Møller et al. 2013) including those in glacier ice (this study), basal ice (Stibal et al., 2012b; Yde et al., 2010), and subglacial waters (Christner et al., 2006; Rondón et al., 2016). Additionally, the warm basal ice contained a large proportion of Chloroflexi (\bar{x} =8.1%) and Gemmatimonadetes (\bar{x} =3.9%), which are common and active in permafrost soils (Tuorto et al., 2014) and other basal ice environments (Yde et al., 2010) but were significantly less dominant in glacier ice samples in this study (Table 1; T-test, $p<0.05$). Warm basal ice also contained relatively few Bacteroidetes (\bar{x} =9.2%) and Cyanobacteria (\bar{x} =0.07%) which were more abundant in glacier ice (Table 1) and in other surface environments (Cameron et al., 2012; Harding et al., 2011).”

Second, it is a bit unfortunate that the only cold-based glacier sampled had a different bedrock type than the three polythermal glaciers, as it makes the differences between the sites more difficult to explain (bedrock vs. thermal regime effect). This should be acknowledged in the relevant sections of the discussion.

Response: Agreed that this is unfortunate and a significant limitation to the study, which is why we attempted to frame the discussion of the warm and cold basal ice by comparing them to meteoric glacier ice rather than directly to each other. Conveniently, the cold basal ice remained remarkably similar to meteoric glacier ice even though it was surrounded by/overlying a more reactive substrate (sandstone, dolomite and limestone) than the warm-based systems (metasedimentary rocks and gneiss). Thus, the warm basal ice acquired more material from a

relatively unreactive substrate while the cold basal ice acquired little material from a reactive substrate. Material on this topic was already integrated in the discussions of “Inorganic nutrients”, “DOM” and “Microbial Assemblages” but additional text was added to the Discussion under ‘Chemistry’ : “The cold basal ice therefore contained solute concentrations and compositions more similar to those in meteoric glacier ice than warm basal ice, even though the substrate beneath the cold-based ice (local sandstone, dolomite, limestone and conglomerate substrate) is likely far more reactive than the substrate beneath the warm-based glaciers (metasedimentary rocks and gneiss). Therefore, the differences in chemistry between these basal environments cannot be explained by differences in substrate alone.”

The text regarding cold basal ice in the conclusion was rewritten to better highlight that the differences in biogeochem can not be fully explained by differences in substrate composition alone: “While basal ice in warm subglacial systems appear to have acquired abundant solutes, microbes and nutrients from the underlying substrate, basal ice produced in cold-based systems acquired few biogeochemical characteristics from the underlying substrate. The cold basal ice explored in this study may have acquired some inorganic and organic nutrients from the substrate, but acquisition of other solutes or microbes appear to be limited. This cold basal ice acquired few solutes and microbes even though the local substrate, composed of sandstone, dolomite and limestone, and relatively well developed soils, would have been more reactive than the metasedimentary and gneiss substrate beneath the warm-based systems.”

Last, there is a discrepancy between DOC (both warm and cold basal ice contained more DOC, including proteinaceous material, compared with meteoric ice) and microbial communities (warm basal ice vs. cold basal ice and meteoric ice). This is in my opinion not sufficiently explained in the ms. Is it because solutes are entrained even by cold-based glaciers but particulates are not? Or may it be an effect of bedrock (see above)?

Response: This research indicates that basal processes in warm-based glaciers result in the acquisition of abundant solutes, microbes and nutrients from the substrate (and possibly from in situ processes), but that cold basal ice appeared to have only acquired specific nutrients from the substrate and not microbes or bulk solutes (even though the substrate was more reactive). We can therefore argue that basal temperature likely plays an important role in controlling subglacial biogeochem. However, identifying the detailed processes that result in the biogeochemical intricacies (and contradictions) of cold-basal ice (ie DOC vs microbes) is beyond the scope of this study - we do not have sufficient information to identify detailed substrate characteristics, mechanism(s) of basal ice formation, or in situ processes that may occur so even speculating in any detail would be unconstrained, and as far as we are concerned, there is no obvious explanation. Instead, we have tweaked the last two sentences of the conclusion to explicitly highlight this the gap in our collective understanding of cold-basal ice biogeochem (and that at this field site) and suggest further research be conducted to help answer these pending and fundamental questions that this research has highlighted: “It remains unknown whether the intricacies of the biogeochemical characteristics that were observed in the cold basal ice in this study result from (i) specific characteristics of the underlying/surrounding substrate, (ii) specific

glaciological/hydrological processes that occurred during the formation of the cold basal ice, or (iii) the effects of biogeochemical processes that occur *in situ* in cold basal ice. Further research is required to define how the cold basal ice at the Western Margin of the DIC developed, and to better characterize the biogeochemical processes that occur in subglacial environments where liquid water is limited.”

Minor comments

260-264 As you didn't specifically look at any microbial functions, the discussion of potential N₂ fixation feels a bit out of place here and could be deleted.

Response: Agreed, so this discussion regarding potential N₂ fixation was deleted

266-289 Emily O'Donnell (Lawson)'s 2016 in BG was the first detailed study on DOM in basal ice and showed e.g. the importance of bedrock and leaching of DOM in wet conditions at the glacier bed. I think it would be a useful reference for this section.

Response: Agreed. The paragraph regarding DOM substrate and microbial DOM sources was revised/expanded to integrate Lawson et al's (2016) findings “Both warm and cold basal ice contained higher average DOC concentrations (0.49 ppm and 0.40 ppm, respectively) than glacier ice (0.15 ppm) (Table 1) suggesting a potential source of DOC in subglacial systems, as observed in Greenland (Lawson et al., 2016) and Antarctica (Wadham et al., 2012)” and “Humic DOM, and humic-like C3 and C5 fluorescence are commonly associated with soils and vegetation (Cory and McKnight, 2005; Osburn et al., 2016; Stedmon et al., 2003) so it is possible that both the fast and slow-flowing glaciers acquired these compounds by direct (via abiotic leaching) and indirect (via microbial cycling) of material from the substrate. Similar observations were made for low molecular weight DOC compounds in previous studies of basal ice from Greenland (Lawson et al., 2016).”

305 Here, the 2012 Global Change Biology paper would be a more appropriate reference, as the experimental data in Wadham et al. come from it (as the first author of this ms surely remembers: :).)

Response: Sincere apologies to the author of this ms – it has been included instead!

323 There already exist spatially explicit studies of microbial communities in glacial environments, mostly the surface – e.g. Cameron et al. 2016 FEMS, Darcy et al. 2017 FEMS. We also found spatial differences in Disko Island glacier stream assemblages (Zarsky et al. 2018 FEMS). These studies might be worth mentioning here.

Response: Thanks for the suggestion – the paragraph was revised to include reference to these studies: “Geographic location has previously been identified as an important determinant of microbial assemblages across various spatial scales, from meters (Lear et al., 2014) to global (Fuhrman et al., 2008), and within other polar environments including Antarctic and Arctic terrestrial and aquatic habitats (Comte et al., 2016; Yergeau et al., 2007) as well as on glacier surfaces (Cameron et al., 2016) and in subglacial discharge (Zarsky et al., 2018).”

Figure 3 seems to show data already shown in Table 1. If this is the case it may be redundant.

Response: Table 1 contains a summary of important and necessary statistical results that are heavily referenced throughout the text. However, it contains a lot of condensed information so is

perhaps difficult for some readers to navigate and discern trends (see comment #7 from Reviewer #2). Therefore Figure 3 was included to provide a visual summary (of scaled results) from which trends can be more easily discerned for the average reader.